

O I P
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SEQUENCE LISTING

<110> Mumper, Russ; Tagliaferri, Frank

<120> HYDROPHOBIC GLYCOSYLMINE DERIVATIVES, COMPOSITIONS, AND METHODS FOR
USE

<130> 237/023

<140> US 09/149,721

<141> 1998-09-08

<150> US 60/058,259

<151> 1997-09-08

<160> 3

<170> Microsoft Word

<210> 1

<211> 462

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (1)...(462)

<223> Coding sequence of human IL-2

<400> 1

atg tac agg atg caa ctc ctg tct tgc att gca cta agt ctt gca ctt 48

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

1

5

10

15

gtc aca aac agt gca cct act tca agt tct aca aag aaa aca cag cta 96

Val Thr Asn Ser Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu

20

25

30

caa ctg gag cat tta ctg ctg gat tta cag atg att ttg aat gga att 144

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile

35

40

45

aat aat tac aag aat ccc aaa ctc acc agg atg ctc aca ttt aag ttt 192
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
50 55 60
tac atg ccc aag aag gcc aca gaa ctg aaa cat ctt cag tgt cta gaa 240
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
65 70 75 80
gaa gaa ctc aaa cct ctg gag gaa gtg cta aat tta gct caa agc aaa 288
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
85 90 95
aac ttt cac tta aga ccc agg gac tta atc agc aat atc aac gta ata 336
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
100 105 110
gtt ctg gaa cta aag gga tct gaa aca aca ttc atg tgt gaa tat gct 384
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
115 120 125
gat gag aca gca acc att gta gaa ttt ctg aac aga tgg att acc ttt 432
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
130 135 140
tgt caa agc atc atc tca aca ctg act tga 462
Cys Gln Ser Ile Ile Ser Thr Leu Thr
145 150
<210> 2
<211> 462
<212> DNA
<213> Artificial Sequence
<220>
<221> CDS
<222> (1)...(462)
<223> Optimized coding sequence of human IL-2

<400> 2

atg tac cgc atg cag ctg ctg agc tgc atc gcc ctg agc ctg gcc ctg 48

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

1 5 10 15

gtg acc aac agc gcc ccc acc agc agc agc acc aag aag acc cag ctg 96

Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu

20 25 30

cag ctg gag cac ctg ctg gac ctg cag atg atc ctg aac ggc atc 144

Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile

35 40 45

aac aac tac aag aac ccc aag ctg acc cgc atg ctg acc ttc aag ttc 192

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe

50 55 60

tac atg ccc aag aag gcc acc gag ctg aag cac ctg cag tgc ctg gag 240

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu

65 70 75 80

gag gag ctg aag ccc ctg gag gag gtg ctg aac ctg gcc cag agc aag 288

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys

85 90 95

aac ttc cac ctg cgc ccc cgc gac ctg atc agc aac atc aac gtg atc 336

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile

100 105 110

gtg ctg gag ctg aag ggc agc gag acc acc ttc atg tgc gag tac gcc 384

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala

115 120 125

gac gag acc gcc acc atc gtg gag ttc ctg aac cgc tgg atc acc ttc 432

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe

130 135 140

tgc cag agc atc atc agc acc ctg acc tga 462

Cys Gln Ser Ile Ile Ser Thr Leu Thr

145 150

<210> 3

<211> 153

<212> PRT

<213> Homo Sapiens

<220>

<223> Amino acid sequence of human IL-2

<400> 3

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

1 5 10 15

Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu

20 25 30

Gln Leu Glu His Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile

35 40 45

Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe

50 55 60

Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu

65 70 75 80

Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys

85 90 95

Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile

100 105 110

Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala

115 120 125

Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe

130 135 140

Cys Gln Ser Ile Ile Ser Thr Leu Thr

145 150